

ABSTRACT

The invention provides several methods of reducing the complexity of a population of nucleic acids prior to performing an analysis of the nucleic acids on a nucleic acid probe array. The methods result in a subset of the initial population enriched for a desired property, or lacking nucleic acids with an undesired property. The resulting nucleic acids in the subset are then applied to the array for various types of analysis. The methods are particularly useful for analyzing populations having a high degree of complexity, for example, populations of fragments spanning a human chromosome, or even a whole human genome, or mRNA populations.

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